SEQUENCE LISTING

<110> Kingsbury, G.
      Leiby, K.

<120> COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
      TREATMENT OF IMMUNE DISORDERS

<130> 7853-158

<140> To be assigned
<141> 2000-04-28

<150> 60/155,862
<151> 1999-09-24

<160> 33

<170> FastSEQ for Windows Version 3.0

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2

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3

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Leu Glu Asn Glu Ala Leu Ile Val Arg Cys Pro Gln Arg Gly Arg Ser
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4

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Leu Pro Ala Arg Val Glu Asp Ser Gly Ile Tyr Ala Cys Val Ile Arg
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Ser Pro Asn Leu Asn Lys Thr Gly Tyr Leu Asn Val Thr Ile His Lys
            100   105   110
Lys Pro Pro Ser Cys Asn Ile Pro Asp Tyr Leu Met Tyr Ser Thr Val
        115   120   125
Arg Gly Ser Asp Lys Asn Phe Lys Ile Thr Cys Pro Thr Ile Asp Leu
    130   135   140
Tyr Asn Trp Thr Ala Pro Val Gln Trp Phe Lys Asn Cys Lys Ala Leu
145   150   155   160
Gln Glu Pro Arg Phe Arg Ala His Arg Ser Tyr Leu Phe Ile Asp Asn
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Val Thr His Asp Asp Glu Gly Asp Tyr Thr Cys Gln Phe Thr His Ala
        180   185   190
Glu Asn Gly Thr Asn Tyr Ile Val Thr Ala Thr Arg Ser Phe Thr Val
        195   200   205
Glu Glu Lys Gly Phe Ser Met Phe Pro Val Ile Thr Asn Pro Pro Tyr
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Asn His Thr Met Glu Val Glu Ile Gly Lys Pro Ala Ser Ile Ala Cys
225   230   235   240
Ser Ala Cys Phe Gly Lys Gly Ser His Phe Leu Ala Asp Val Leu Trp
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Gln Ile Asn Lys Thr Val Val Gly Asn Phe Gly Glu Ala Arg Ile Gln
            260   265   270
Glu Glu Glu Gly Arg Asn Glu Ser Ser Ser Asn Asp Met Asp Cys Leu
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Thr Ser Val Leu Arg Ile Thr Gly Val Thr Glu Lys Asp Leu Ser Leu
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Glu Tyr Asp Cys Leu Ala Leu Asn Leu His Gly Met Ile Arg His Thr
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Ala

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        <212> PRT
        <213> Mus musculus

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        35   40   45
Thr Tyr Pro Val Glu Trp Tyr Tyr Ser Asp Thr Asn Glu Ser Ile Pro
    50   55   60
Thr Gln Lys Arg Asn Arg Ile Phe Val Ser Arg Asp Arg Leu Lys Phe
65   70   75   80
Leu Pro Ala Arg Val Glu Asp Ser Gly Ile Tyr Ala Cys Val Ile Arg
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5

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Lys Pro Pro Ser Cys Asn Ile Pro Asp Tyr Leu Met Tyr Ser Thr Val
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Arg Gly Ser Asp Lys Asn Phe Lys Ile Thr Cys Pro Thr Ile Asp Leu
        130               135               140
Tyr Asn Trp Thr Ala Pro Val Gln Trp Phe Lys Asn Cys Lys Ala Leu
145               150               155               160
Gln Glu Pro Arg Phe Arg Ala His Arg Ser Tyr Leu Phe Ile Asp Asn
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Val Thr His Asp Asp Glu Gly Asp Tyr Thr Cys Gln Phe Thr His Ala
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Glu Asn Gly Thr Asn Tyr Ile Val Thr Ala Thr Arg Ser Phe Thr Val
            195               200               205
Glu Glu Lys Gly Phe Ser Met Phe Pro Val Ile Thr Asn Pro Pro Tyr
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Asn His Thr Met Glu Val Glu Ile Gly Lys Pro Ala Ser Ile Ala Cys
225               230               235               240
Ser Ala Cys Phe Gly Lys Gly Ser His Phe Leu Ala Asp Val Leu Trp
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Ser Val Glu Tyr Phe Val His His Thr Leu Pro Asp Val Leu Glu Asn
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Gln Val Phe Val Leu Ala Pro His Met Met His Ser Lys Glu Phe Ala
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Tyr Glu Gln Glu Ile Ala Leu His Ser Ala Leu Ile Gln Asn Asn Ser
465               470               475               480
Lys Val Ile Leu Ile Glu Met Glu Pro Leu Gly Glu Ala Ser Arg Leu
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Gln Val Gly Asp Leu Gln Asp Ser Leu Gln His Leu Val Lys Ile Gln
            500               505               510
Gly Thr Ile Lys Trp Arg Glu Asp His Val Ala Asp Lys Gln Ser Leu
            515               520               525
Ser Ser Lys Phe Trp Lys His Val Arg Tyr Gln Met Pro Val Pro Glu
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6

Cys Leu Asp Leu Lys His Phe
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<211> 556
<212> PRT
<213> Homo sapiens

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Ile Val Arg Cys Pro Arg Gln Gly Lys Pro Ser Tyr Thr Val Asp Trp
            35   40   45
Tyr Tyr Ser Gln Thr Asn Lys Ser Ile Pro Thr Gln Glu Arg Asn Arg
 50   55   60
Val Phe Ala Ser Gly Gln Leu Leu Lys Phe Leu Pro Ala Glu Val Ala
 65   70   75   80
Asp Ser Gly Ile Tyr Thr Cys Ile Val Arg Ser Pro Thr Phe Asn Arg
                85   90   95
Thr Gly Tyr Ala Asn Val Thr Ile Tyr Lys Lys Gln Ser Asp Cys Asn
                100   105   110
Val Pro Asp Tyr Leu Met Tyr Ser Thr Val Ser Gly Ser Glu Lys Asn
            115   120   125
Ser Lys Ile Tyr Cys Pro Thr Ile Asp Leu Tyr Asn Trp Thr Ala Pro
    130   135   140
Leu Glu Trp Phe Lys Asn Cys Gln Ala Leu Gln Gly Ser Arg Tyr Arg
145   150   155   160
Ala His Lys Ser Phe Leu Val Ile Asp Asn Val Met Thr Glu Asp Ala
                165   170   175
Gly Asp Tyr Thr Cys Lys Phe Ile His Asn Glu Asn Gly Ala Asn Tyr
                180   185   190
Ser Val Thr Ala Thr Arg Ser Phe Thr Val Lys Asp Glu Gln Gly Phe
            195   200   205
Ser Leu Phe Pro Val Ile Gly Ala Pro Ala Gln Asn Glu Ile Lys Glu
    210   215   220
Val Glu Ile Gly Lys Asn Ala Asn Leu Thr Cys Ser Ala Cys Phe Gly
225   230   235   240
Lys Gly Thr Gln Phe Leu Ala Ala Val Leu Trp Gln Leu Asn Gly Thr
                245   250   255
Lys Ile Thr Asp Phe Gly Glu Pro Arg Ile Gln Gln Glu Glu Gly Gln
                260   265   270
Asn Gln Ser Phe Ser Asn Gly Leu Ala Cys Leu Asp Met Val Leu Arg
            275   280   285
Ile Ala Asp Val Lys Glu Glu Asp Leu Leu Leu Gln Tyr Asp Cys Leu
    290   295   300
Ala Leu Asn Leu His Gly Leu Arg Arg His Thr Val Arg Leu Ser Arg
305   310   315   320
Lys Asn Pro Ile Asp His His Ser Ile Tyr Cys Ile Ile Ala Val Cys
                325   330   335
Ser Val Phe Leu Met Leu Ile Asn Val Leu Val Ile Ile Leu Lys Met
            340   345   350
Phe Trp Ile Glu Ala Thr Leu Leu Trp Arg Asp Ile Ala Lys Pro Tyr
    355   360   365
Lys Thr Arg Asn Asp Gly Lys Leu Tyr Asp Ala Tyr Val Val Tyr Pro
    370   375   380

7

```
Arg Asn Tyr Lys Ser Ser Thr Asp Gly Ala Ser Arg Val Glu His Phe
385                 390                 395                 400
Val His Gln Ile Leu Pro Asp Val Leu Glu Asn Lys Cys Gly Tyr Thr
                405             410             415
Leu Cys Ile Tyr Gly Arg Asp Met Leu Pro Gly Glu Asp Val Val Thr
            420             425             430
Ala Val Glu Thr Asn Ile Arg Lys Ser Arg Arg His Ile Phe Ile Leu
        435             440             445
Thr Pro Gln Ile Thr His Asn Lys Glu Phe Ala Tyr Glu Gln Glu Val
    450             455             460
Ala Leu His Cys Ala Leu Ile Gln Asn Asp Ala Lys Val Ile Leu Ile
465             470             475             480
Glu Met Glu Ala Leu Ser Glu Leu Asp Met Leu Gln Ala Glu Ala Leu
            485             490             495
Gln Asp Ser Leu Gln His Leu Met Lys Val Gln Gly Thr Ile Lys Trp
            500             505             510
Arg Glu Asp His Ile Ala Asn Lys Arg Ser Leu Asn Ser Lys Phe Trp
    515             520             525
Lys His Val Arg Tyr Gln Met Pro Val Pro Ser Lys Ile Pro Arg Lys
    530             535             540
Ala Ser Ser Leu Thr Pro Leu Ala Ala Gln Lys Gln
545             550             555
```

        <210> 9
        <211> 328
        <212> PRT
        <213> Homo sapiens

        <400> 9

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Met Gly Phe Trp Ile Leu Ala Ile Leu Thr Ile Leu Met Tyr Ser Thr
1               5               10              15
Ala Ala Lys Phe Ser Lys Gln Ser Trp Gly Leu Glu Asn Glu Ala Leu
            20              25              30
Ile Val Arg Cys Pro Arg Gln Gly Lys Pro Ser Tyr Thr Val Asp Trp
            35              40              45
Tyr Tyr Ser Gln Thr Asn Lys Ser Ile Pro Thr Gln Glu Arg Asn Arg
    50              55              60
Val Phe Ala Ser Gly Gln Leu Leu Lys Phe Leu Pro Ala Glu Val Ala
65              70              75              80
Asp Ser Gly Ile Tyr Thr Cys Ile Val Arg Ser Pro Thr Phe Asn Arg
            85              90              95
Thr Gly Tyr Ala Asn Val Thr Ile Tyr Lys Lys Gln Ser Asp Cys Asn
            100             105             110
Val Pro Asp Tyr Leu Met Tyr Ser Thr Val Ser Gly Ser Glu Lys Asn
    115             120             125
Ser Lys Ile Tyr Cys Pro Thr Ile Asp Leu Tyr Asn Trp Thr Ala Pro
    130             135             140
Leu Glu Trp Phe Lys Asn Cys Gln Ala Leu Gln Gly Ser Arg Tyr Arg
145             150             155             160
Ala His Lys Ser Phe Leu Val Ile Asp Asn Val Met Thr Glu Asp Ala
            165             170             175
Gly Asp Tyr Thr Cys Lys Phe Ile His Asn Glu Asn Gly Ala Asn Tyr
            180             185             190
Ser Val Thr Ala Thr Arg Ser Phe Thr Val Lys Asp Glu Gln Gly Phe
    195             200             205
Ser Leu Phe Pro Val Ile Gly Ala Pro Ala Gln Asn Glu Ile Lys Glu
    210             215             220
```

8

```
Val Glu Ile Gly Lys Asn Ala Asn Leu Thr Cys Ser Ala Cys Phe Gly
225                 230             235             240
Lys Gly Thr Gln Phe Leu Ala Ala Val Leu Trp Gln Leu Asn Gly Thr
            245             250             255
Lys Ile Thr Asp Phe Gly Glu Pro Arg Ile Gln Gln Glu Glu Gly Gln
            260             265             270
Asn Gln Ser Phe Ser Asn Gly Leu Ala Cys Leu Asp Met Val Leu Arg
        275             280             285
Ile Ala Asp Val Lys Glu Glu Asp Leu Leu Leu Gln Tyr Asp Cys Leu
        290             295             300
Ala Leu Asn Leu His Gly Leu Arg Arg His Thr Val Arg Leu Ser Arg
305             310             315             320
Lys Asn Pro Ser Lys Glu Cys Phe
                325
```

```
    <400> 10
cttagctccg tcactgactc caagttcatc ccctctgtct ttcagtttgg ttgagatata    60
ggctactctt cccaactcag tcttgaagag tatcaccaac tgcctcatgt gtggtgacct   120
tcactgttgt atgccagtga ctcatctgga gtaatctcaa caacgagtta ccaatacttg   180
ctcttgattg ataaacagaa tggggttttg gatcttagca attctcacaa ttctcatgta   240
ttccacagca gcaaagttta gtaaacaatc atggggcctg gaaatgagg cttttaattgt   300
aagatgtcct agacaaggaa aacctagtta caccgtggat tggtattact cacaaacaaa   360
caaaagtatt cccactcagg aaagaaatcg tgtgtttgcc tcaggccgac ttctgaagtt   420
tctaccagct gaagttgctg attctggtat ttatacctgt attgtcagaa gtcccacatt   480
caataggact ggatatgcga atgtcaccat atataaaaaa caatcagatt gcaatgttcc   540
agattatttg atgtattcaa cagtatctgg atcagaaaaa aattccaaaa tttattgtcc   600
taccattgac ctctacaact ggacagcacc tcttgagtgg tttaagaatt gtcaggctct   660
tcaaggatca aggtacaggg cgcacaagtc atttttggtc attgataatg tgatgactga   720
ggacgcaggt gattacacct gtaaatttat acacaatgaa aatggagcca attatagtgt   780
gacggcgacc aggtccttca cggtcaaggt ttggtgtcag agtttctgca aattaaaaaa   840
gagcttaatc tttagtaata ctcattggat tcaaagtcta atgagaggct ttgtgatggt   900
atactatggt gtacataaat gttgtcgagt ggttttttaat ctttgtttgc aatactttca   960
acatcatcaa tggccttgaa tgagcaaggc ttttctctgt ttccagtaat cggagcccct  1020
gcacaaaatg aaataaagga agtggaaatt ggaaaaaacg caaacctaac ttgctctgct  1080
tgttttggaa aaggcactca gttcttggct gccgtcctgt ggcagcttaa tggaacaaaa  1140
attacagact ttggtgaacc aagaattcaa caagaggaag ggcaaaatca aagtttcagc  1200
aatgggctgg cttgtctaga catggtttta agaatagctg acgtgaagga agaggattta  1260
ttgctgcagt acgactgtct ggccctgaat ttgcatggct tgagaaggca caccgtaaga  1320
ctaagtagga aaaatccaag taaggagtgt ttctgagact ttgatcacct gaactttctc  1380
tagcaagtgt aagcagaatg gagtgtggtt ccaagagatc catcaagaca atgggaatgg  1440
cctgtgccat aaaatgtgct tctcttcttc gggatgttgt ttgctgtctg atctttgtag  1500
actgttcctg tttgctggga gcttctctgc tgcttaaatt gttcgtcctc ccccactccc  1560
tcctatcgtt ggtttgtcta gaacactcag ctgcttcttt ggtcatcctt gttttctaac  1620
tttatgaact ccctctgtgt cactgtatgt gaaaggaaat gcaccaacaa ccgaaaactg  1680
```

```
    <400> 11
Met Gly Phe Trp Ile Leu Ala Ile Leu Thr Ile Leu Met Tyr Ser Thr
 1           5               10              15
```

9

```
Ala Ala Lys Phe Ser Lys Gln Ser Trp Gly Leu Glu Asn Glu Ala Leu
            20                  25                  30
Ile Val Arg Cys Pro Arg Gln Gly Lys Pro Ser Tyr Thr Val Asp Trp
        35                  40                  45
Tyr Tyr Ser Gln Thr Asn Lys Ser Ile Pro Thr Gln Glu Arg Asn Arg
    50                  55                  60
Val Phe Ala Ser Gly Arg Leu Leu Lys Phe Leu Pro Ala Glu Val Ala
65                  70                  75                  80
Asp Ser Gly Ile Tyr Thr Cys Ile Val Arg Ser Pro Thr Phe Asn Arg
                85                  90                  95
Thr Gly Tyr Ala Asn Val Thr Ile Tyr Lys Lys Gln Ser Asp Cys Asn
            100                 105                 110
Val Pro Asp Tyr Leu Met Tyr Ser Thr Val Ser Gly Ser Glu Lys Asn
        115                 120                 125
Ser Lys Ile Tyr Cys Pro Thr Ile Asp Leu Tyr Asn Trp Thr Ala Pro
    130                 135                 140
Leu Glu Trp Phe Lys Asn Cys Gln Ala Leu Gln Gly Ser Arg Tyr Arg
145                 150                 155                 160
Ala His Lys Ser Phe Leu Val Ile Asp Asn Val Met Thr Glu Asp Ala
                165                 170                 175
Gly Asp Tyr Thr Cys Lys Phe Ile His Asn Glu Asn Gly Ala Asn Tyr
            180                 185                 190
Ser Val Thr Ala Thr Arg Ser Phe Thr Val Lys Val Trp Cys Gln Ser
            195                 200                 205
Phe Cys Lys Leu Lys Lys Ser Leu Ile Phe Ser Asn Thr His Trp Ile
    210                 215                 220
Gln Ser Leu Met Arg Gly Phe Val Met Val Tyr Tyr Gly Val His Lys
225                 230                 235                 240
Cys Cys Arg Val Val Phe Asn Leu Cys Leu Gln Tyr Phe Gln His His
            245                 250                 255
Gln Trp Pro


    <210> 12
    <211> 1210
    <212> DNA
    <213> Homo sapiens

    <220>
    <221> CDS
    <222> (84)...(557)

    <400> 12
gtcgacccac gcgtccgccc acgcgtccgc tggagtaatc tcaacaacga gttaccaata      60
cttgctcttg attgataaac aga atg ggg ttt tgg atc tta gca att ctc aca     113
                         Met Gly Phe Trp Ile Leu Ala Ile Leu Thr
                          1               5                   10

att ctc atg tat tcc aca gca gca aag ttt agt aaa caa tca tgg ggc      161
Ile Leu Met Tyr Ser Thr Ala Ala Lys Phe Ser Lys Gln Ser Trp Gly
            15                  20                  25

ctg gaa aat gag gct tta att gta aga tgt cct aga caa gga aaa cct      209
Leu Glu Asn Glu Ala Leu Ile Val Arg Cys Pro Arg Gln Gly Lys Pro
        30                  35                  40
```

10

```
agt tac acc gtg gat tgg tat tac tca caa aca aac aaa agt att ccc        257
Ser Tyr Thr Val Asp Trp Tyr Tyr Ser Gln Thr Asn Lys Ser Ile Pro
        45                      50                      55

act cag gaa aga aat cgt gtg ttt gcc tca ggc caa ctt ctg aag ttt        305
Thr Gln Glu Arg Asn Arg Val Phe Ala Ser Gly Gln Leu Leu Lys Phe
        60                      65                      70

cta cca gct gca gtt gct gat tct ggt att tat acc tgt att gtc aga        353
Leu Pro Ala Ala Val Ala Asp Ser Gly Ile Tyr Thr Cys Ile Val Arg
75                      80                      85                      90

agt ccc aca ttc aat agg act gga tat gcg aat gtc acc ata tat aaa        401
Ser Pro Thr Phe Asn Arg Thr Gly Tyr Ala Asn Val Thr Ile Tyr Lys
                        95                      100                     105

aaa caa tca gat tgc aat gtt cca gat tat ttg atg tat tca aca gta        449
Lys Gln Ser Asp Cys Asn Val Pro Asp Tyr Leu Met Tyr Ser Thr Val
                110                     115                     120

tct gga tca gaa aaa aat tcc aaa att tat tgt cct acc att gac ctc        497
Ser Gly Ser Glu Lys Asn Ser Lys Ile Tyr Cys Pro Thr Ile Asp Leu
            125                     130                     135

tac aac tgg aca gca cct ctt gag tgg ttt aag atg agc aag gct ttt        545
Tyr Asn Trp Thr Ala Pro Leu Glu Trp Phe Lys Met Ser Lys Ala Phe
        140                     145                     150

ctc tgt ttc cag taatcggagc ccctgcacaa aatgaaataa aggaagtgga           597
Leu Cys Phe Gln
155


aattggcact cagttcttgg ctgccgtcct gtggcagctt aatggaacaa aaattacaga     657
ctttggtgaa ccaagaattc aacaagagga agggcaaaat caaagtttca gcaatgggct     717
ggcttgtcta gacatggttt taagaatagc tgacgtgaag gaagaggatt tattgctgca     777
gtacgactgt ctggccctga atttgcatgg cttgagaagg cacaccgtaa gactaagtag     837
gaaaaatcca agtaggagt gtttctgaga ctttgatcac ctgaactttc tctagcaagt      897
gtaagcagaa tggagtgtgg ttccaagaga tccatcaaga caatgggaat ggcctgtgcc     957
ataaaatgtg cttctcttct tcgggatgtt gtttgctgtc tgatctttgt agactgttcc     1017
tgtttgctgg gagcttctct gctgcttaaa ttgttcgtcc tcccccactc cctcctatcg     1077
ttggtttgtc tagaacactc agctgcttct ttggtcatcc ttgttttcta actttatgaa     1137
ctccctctgt gtcactgtat gtgaaaggaa atgcaccaac aaccgtaaaa aaaaaaaaa      1197
aagggcggcc gct                                                         1210


        <210> 13
        <211> 158
        <212> PRT
        <213> Homo sapiens


        <400> 13
Met Gly Phe Trp Ile Leu Ala Ile Leu Thr Ile Leu Met Tyr Ser Thr
1               5                       10                      15
Ala Ala Lys Phe Ser Lys Gln Ser Trp Gly Leu Glu Asn Glu Ala Leu
                20                      25                      30
Ile Val Arg Cys Pro Arg Gln Gly Lys Pro Ser Tyr Thr Val Asp Trp
            35                      40                      45
Tyr Tyr Ser Gln Thr Asn Lys Ser Ile Pro Thr Gln Glu Arg Asn Arg
        50                      55                      60
```

11

```
Val Phe Ala Ser Gly Gln Leu Leu Lys Phe Leu Pro Ala Ala Val Ala
65                   70                  75                  80
Asp Ser Gly Ile Tyr Thr Cys Ile Val Arg Ser Pro Thr Phe Asn Arg
                85                  90                  95
Thr Gly Tyr Ala Asn Val Thr Ile Tyr Lys Lys Gln Ser Asp Cys Asn
            100                 105                 110
Val Pro Asp Tyr Leu Met Tyr Ser Thr Val Ser Gly Ser Glu Lys Asn
        115                 120                 125
Ser Lys Ile Tyr Cys Pro Thr Ile Asp Leu Tyr Asn Trp Thr Ala Pro
    130                 135                 140
Leu Glu Trp Phe Lys Met Ser Lys Ala Phe Leu Cys Phe Gln
145                 150                 155
```

            <210> 14
            <211> 18
            <212> DNA
            <213> Artificial Sequence

            <220>
            <223> sense primer

            <400> 14
ttgccataga gagacctc   18

            <210> 15
            <211> 19
            <212> DNA
            <213> Artificial Sequence

            <220>
            <223> antisense primer

            <400> 15
tgctgtccaa ttatacagg   19

            <210> 16
            <211> 22
            <212> DNA
            <213> Artificial Sequence

            <220>
            <223> sense primer

            <400> 16
gaacacggca ttgtcactaa ct   22

            <210> 17
            <211> 21
            <212> DNA
            <213> Artificial Sequence

            <220>
            <223> antisense primer

            <400> 17
cctcatagat gggcactgtg t   21

            <210> 18

12

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<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> forward primer

<400> 18
tgtgacggcg accaggt                                                          17


<210> 19
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> reverse primer

<400> 19
tctctgtttc cagtaatcgg agc                                                   23


<210> 20
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> TaqMan probe

<400> 20
ttcacggtca aggatgagca agcctt                                                26


<210> 21
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> forward primer

<400> 21
cacccccact gaaaaagatg a                                                     21


<210> 22
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> reverse primer

<400> 22
cttaactatc ttgggctgtg acaaag                                                26


<210> 23
<211> 24
<212> DNA
<213> Artificial Sequence
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<220>
<223> TaqMan probe

<400> 23
tatgcctgcc gtgtgaacca cgtg   24

<210> 24
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> 5' oligonucleotide

<400> 24
ccgcgggtac cagtaaatcg tcctggggtg g   31

<210> 25
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> 3' oligonucleotide

<400> 25
aaataaagga tccctacatc cagcaactat gtagta   36

<210> 26
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> 5' oligonucleotide

<400> 26
gaacacacta gtactatcct gtgccattgc catagaga   38

<210> 27
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> 3' oligonucleotide

<400> 27
ggaatattgg gcccttggat cccaagtctg cacacctgca ctcc   44

<210> 28
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> 5' oligonucleotide

```
<400> 28
gtaaatcgtc ctggggtctg g                                                    21

        <210> 29
        <211> 25
        <212> DNA
        <213> Artificial Sequence

        <220>
        <223> 3' oligonucleotide

        <400> 29
ccttctgata acacaagcat aaatc                                                25

        <210> 30
        <211> 17
        <212> DNA
        <213> Artificial Sequence

        <220>
        <223> primer

        <400> 30
acggagggca gtaaatc                                                         17

        <210> 31
        <211> 18
        <212> DNA
        <213> Artificial Sequence

        <220>
        <223> primer

        <400> 31
cagccaagaa gtgagagc                                                        18

        <210> 32
        <211> 22
        <212> DNA
        <213> Artificial Sequence

        <220>
        <223> primer

        <400> 32
tgttgccgga atccagcctc ag                                                   22

        <210> 33
        <211> 23
        <212> DNA
        <213> Artificial Sequence

        <220>
        <223> primer

        <400> 33
gtcccccacc cccagataca acc                                                  23
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